of X_8 and Y_8 share homology with the NBRE sequence defined by nucleotide the hexanucleotide sequence AGGTCA, and its complement TGACCT, respectively, and wherein said response element is capable of binding to a dimer consisting of two partners which are selected from members of the Nur family of nuclear receptors.

23. The oligonucleotide sequence of claim 22, wherein 4 out of 6 nucleotides of N_6 are identical to said AGGTCA or TGACCT sequences.

24. The oligonucleotide sequence of claim 23, wherein AAN_6 has a sequence selected from the group consisting of AAATATCA, AAATGCCA, AAAGGTCA, and functional derivatives thereof.

25. The oligonucleotide sequence of claim 23, wherein N_6TT has a sequence selected from the group consisting of TGATATTT, TGGCATTT, TGACCTTT, and functional derivatives thereof.

26. The oligonucleotide sequence of claim 25, wherein said response element comprises a nucleotide sequence selected from the group consisting of :

GTGATATTTXXXXXXAAATGCCAG, TGATATTTXXXXXXAAATGCCA, GTGATATTTXXXXXXAAATATCAC, TGATATTTXXXXXXAAATATCA, CTGGCATTTXXXXXXAAATGCCAG, TGGCATTTXXXXXXAAATGCCA, QTGACCTTTXXXXXXAAAGGTCAQ, TGACCTTTXXXXXXAAAGGTCA, QTGUYATTTXXXXXXAAATUYCAQ,TGUYATTTXXXXXXAAATUYCA, GTGATATTTACCTCCAAATGCCAG, TGATATTTACCTCCAAATGCCA, GTGATATTTACCTCCAAATATCAC, TGATATTTACCTCCAAATATCA, CTGGCATTTACCTCCAAATGCCAG, TGGCATTTACCTCCAAATGCCA,

QTGACCTTTACCTCCAAAGGTCAQ, TGACCTTTACCTCCAAAGGTCA, QTGUYATTTACCTCCAAATUYCAQ,TGUYATTTACCTCCAAATUYCA, complements and functional derivatives thereof, wherein X is independently selected from A,T,C,or G, U is a purine, Y is a pyrimidine, and Q is C or G.

27. The oligonucleotide sequence of claim 26, wherein said response element comprises a nucleic acid sequence selected from the group consisting of: GTGATATTTXXXXXXAAATGCCAG and TGACCTTTXXXXXXAAAGGTCA.

28. The oligonucleotide sequence of claim 27, wherein said response element comprises nucleic acid sequence TGATATTTACCTCCAAATGCCA.

29. The oligonucleotide sequence of claim 28, wherein said response element comprises nucleic acid sequence GTGATATTTACCTCCAAATGCCAG.

30. The oligonucleotide sequence of claim 27, wherein said response element comprises nucleic acid sequence TGACCTTTXXXXXXAAAGGTCA.

31. The oligonucleotide sequence of claim 22, wherein said member of the Nur family of nuclear receptors is selected from the group consisting of: Nur77, NGFI-B, N10, NAK1, TR3, Nurr-1, RNR-1, NOT, TINUR, NOR-1 and MINOR.

32. The oligonucleotide sequence of claim 22, wherein said response element binds to a homodimer consisting of two partners of the same member of the Nur family of nuclear receptors.

33. The oligonucleotide sequence of claim 22, wherein said response element binds to a heterodimer consisting of two partners of a different member of the Nur family of nuclear receptors.

34. A DNA construct comprising the oligonucleotide sequence of claim 22, operably linked to a promoter, which promoter is operably linked to a heterologous gene, wherein the DNA construct is linked in such a manner that the gene is under the transcriptional control of the oligonucleotide sequence and promoter.

35. The DNA construct of claim 34, wherein said oligonucleotide sequence comprises a multimer of at least one of said response element.

36. The DNA construct of claim 34, wherein the heterologous gene is a reporter gene.

37. A host cell transfected with the DNA construct of claim 34.

38. A method for controlled expression of a heterologous gene of interest comprising culturing a host cell according to claim 37 in the presence of an appropriate regulatory protein.

39. The method according to claim 38, wherein the regulatory protein comprises a member of the Nur family of nuclear receptors.

40. A method for detecting a modulator of transcription at a Nur response element (Nur-RE), wherein said Nur-RE is an oligonucleotide sequence comprising a response element that binds to a nuclear receptor of the Nur family of nuclear receptors, said response element comprising nucleotide sequence X_8 L_6 Y_8, wherein:

a) X_8 and Y_8 are two half site sequences of 8 nucleotides which are configured as an everted repeat;

b) L_6 separates said half site sequences, with L being 6 nucleotides and being independently selected from A,T,C,or G;

c) X_8 having nucleotide sequence N_6TT, and Y_8 having nucleotide sequence AAN_6, wherein N is selected from A,T,C,or G, such that said sequence of X_8 and Y_8 share homology with the NBRE sequence defined by nucleotide the hexanucleotide sequence AGGTCA, and its complement TGACCT, respectively, and wherein said response element is capable of binding to a dimer consisting of two partners which are selected from members of the Nur family of nuclear receptors ,

comprising contacting a sample with said host cell according to claim 37, and comparing the level of expression of said reporter gene in the presence of the sample and in the absence thereof.

41. A method for measuring the ability of a compound to modulate transcription at a Nur response element (Nur-RE), wherein said Nur-RE is an oligonucleotide sequence comprising a response element that binds to a nuclear receptor of the Nur family of nuclear receptors, said response element comprising nucleotide sequence X_8 L_6 Y_8, wherein:

a) X_8 and Y_8 are two half site sequences of 8 nucleotides which are configured as an everted repeat;

b) L_6 separates said half site sequences, with L being 6 nucleotides and being independently selected from A,T,C,or G;

c) X_8 having nucleotide sequence N_6TT, and Y_8 having nucleotide sequence AAN_6, wherein N is selected from A,T,C,or G, such that said sequence of X_8 and Y_8 share homology with the NBRE sequence defined by nucleotide the hexanucleotide sequence AGGTCA, and its complement TGACCT, respectively, and wherein said response element is capable of binding to a dimer consisting of two partners which are selected from members of the Nur family of nuclear receptors ,

comprising:

a) contacting said compound with said host cell of claim 37, under conditions conducive to the expression of said heterologous gene in response to said compound; and

b) comparing the level of gene expression in step a) with the level of gene expression from said host cell in the absence of said compound.

42. The method of claim 41 to identify a ligand selective for Nur family transcriptional complexes.

43. An isolated multimeric complex comprising at least a dimer consisting of two partners which are selected from members of the Nur family of nuclear receptors.

44. The multimeric complex of claim 43, wherein said dimer is a homodimer consisting of two partners of the same member of the Nur family of nuclear receptors.

45. The multimeric complex of claim 43, wherein said dimer is a heterodimer consisting of two partners of a different member of the Nur family of nuclear receptors.